# Haplogroup I-Y17672 in a Genealogical DNA Dataset: Discrepancies in Y-Chromosome TMRCA Estimation Across Testing Platforms

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## Background

"The Tipton Family DNA Project (TFDP) originally began as a way to determine if and how Thomas Tipton who resided in Burke County, Georgia, from 1785 to about 1820 connected to the Tiptons who descend from Jonathan Tipton who died in Baltimore County, Maryland, in 1757."[1] To date, significant contributions have been made to the TFDP,[2] hosted in part by FamilyTree DNA (FTDNA). The first aspect of the project utilized autosomal-DNA testing to ascertain Oldest Common Ancestor (OCA). The second aspect, the Tipton Family Y-DNA (T-YDP) project, currently includes 111 participants of which an appreciable number align to haplogroups I-M253, I-Y17672, and I-Y17673. I-Y17672 is a branch of I-M253 and I-Y17673 is a branch of I-Y17672. Further subclades have been grouped beyond I-Y17673. The TFDP is working towards connecting recent generations confirmed by autosomal-DNA with prior generations predicted by Y-DNA testing. This analysis aims to further the work that was shared with The Tipton Family Association in 2022[3] by assessing the latest data from the TFDP, the Debenham Y-DNA Project (D-YDP), and the YFull Y-DNA Database.

## Methods

In this cross-sectional secondary data analysis (SDA), four publicly available datasets were evaluated: the autosomal-DNA results of the TFDP published in the Tipton Family Association newsletter in 2022, the two current T-YDP and D-YDPs published by FTDNA, and the YFull Y-DNA Database. The T-YDP and D-YDP datasets were given equal weight through equal inclusion per eligible participant, as all included samples met the same Y-DNA testing resolution and haplogroup criteria. Years Before Present (YBP) values in the dataset were converted using the standard convention of Present = 1950 Common Era (CE) to enable comparison between testing companies. Haplogroup dating with uncertainty exceeding the 95% confidence threshold was excluded.

The SDA Y-DNA analysis population began with 147 current participants in the T-YDP and D-YDPs, of which 24 met eligibility within subclade I-Y17672 and were evaluated.

Those who tested outside the I-M253 haplogroup, which contains the subclades of interest, were first excluded. There are 39 men included in the T-YDP and 4 men in the D-YDP analysis who have tested to a specificity of I-M253. "Haplogroup I-M253, also known as I1, is a Y chromosome haplogroup."[4] "Haplogroup I1 is believed to have been present among Upper Paleolithic European hunter-gatherers as a minor lineage but due to its near-total absence in pre-Neolithic DNA samples, it cannot have been very

[1] FamilyTree DNA. (n.d.). Tipton Family DNA Project. Retrieved September 1, 2025, from https://www.familytreedna.com/groups/tipton/dna-results
[2] Ibid.
[3] The Tipton Family Association of America. (2022). *The Tipton Family Association of America Newsletter, Issue 44*. Retrieved from https://tiptonfamilyassociationofamerica.com/wp-content/uploads/2022/12/Newsletter44_Fall_2022.pdf
[4] Y-DNA Haplogroup I and its Subclades. (n.d.). Retrieved August 31, 2025, from https://discover.familytreedna.com/y-dna/I-M253/storyhttps://isogg.org/tree/ISOGG_HapgrpI.html

widespread. Neolithic I1 samples are very sparse as well, suggesting a rapid dispersion connected to a founder effect in the Nordic Bronze Age. Today it reaches its peak frequencies in Sweden (52 percent of males in Västra Götaland County) and western Finland (more than 50 percent in Satakunta province)."[5] When accessed in 2025, 76,133 men had tested positive for I-M253 on the FTDNA platform and had been assigned to projects organized by surname. Their current locations being "Sweden 5,369, England 4,200, United States 3,332, and Other Countries 63,232."[6] Because these participants match such a broad population of men from numerous countries in the FTDNA database, they do not meaningfully inform the TFDP's specific genealogical research question and were therefore excluded from analysis.

Finally, participants who did not furnish their oldest paternal ancestor by genealogical research were excluded.

Results were generated using Microsoft Office 365 tools. All TFDP information used in this analysis was drawn from publicly available sources and was further anonymized for reporting. Participants in the T-YDP and D-YDP projects had explicitly opted to make portions of their pseudonymized Y-DNA data publicly accessible by joining the projects. All data included in this study therefore originates from individuals who consented to public sharing through these genealogical platforms. No confidential, private, or non-public information was accessed.

## Results

Table 1: Haplogroup I-Y17672 Surname Frequency

| Surname | Frequency |
|---|---|
| Tipton | 79.17% |
| Deadman | 8.33% |
| Foster | 4.17% |
| Garretson | 4.17% |
| Phillips | 4.17% |

(n=24)

[5] Lappalainen T, Laitinen V, Salmela E, Andersen P, Huoponen K, Savontaus ML, Lahermo P (May 2008). "Migration waves to the Baltic Sea region". *Annals of Human Genetics*. **72** (Pt 3): 337–348. doi:10.1111/j.1469-1809.2007.00429.x. PMID 18294359. S2CID 3207990

[6] FamilyTree DNA. (n.d.). Your Haplogroup Story: I-M253. Retrieved August 31, 2025, from https://discover.familytreedna.com/y-dna/I-M253/story

## Discussion

The autosomal-DNA proven OCAs from the TFDP were accepted as autosomal-DNA testing has a high degree of reliability within the five most recent generations. Autosomal-DNA testing employs SNP microarrays to test ~600,000–700,000 genetic markers. Repeat testing with labs yields raw data that is nearly identical apart from negligible lab error rates (<0.1%). In the case of testing with different labs, due to slightly different test designs, results are not perfect, but yield significantly overlapping SNPs.

West's work in the TFDP determining OCAs via autosomal testing has established a solid foundation supporting the traditional genealogical research of the Tipton family. While limitations of autosomal-DNA testing include the likelihood of false positives with segments <7 CM, the influence of endogamy falsely shortening the distance of matches, and employing the approach absent a proper documented genealogy, the Tipton genealogies are robust and the approach repeatable. Bridging the gap between this research and the Y-DNA research presents a significant challenge as no genealogically proven Tipton male born prior to 1925 has been Y-DNA tested. Consequently, hypotheses of descent beyond autosomal-DNA proven OCAs must be expressed as probabilities rather than certainties.

### Y-DNA Time to the Most Recent Common Ancestor (TMRCA) Controversy

There are two broad approaches to establishing TMRCA, the first being Evolutionary Mutation Rates based on using long-term timescales which result in estimates often thousands of years earlier than other models and the second being Genealogical Mutation Rates which are based on observed mutations in known genealogies. Academic and Genealogical research communities do not agree on which method is most accurate. In fact, some researchers advocate for a hybrid approach.

FTDNA presently uses a time predictor, reliant on a combination of Y-chromosome Short Tandem Repeat (STR) genetic distance and Y-chromosome Single Nucleotide Polymorphism (SNP) data to estimate the TMRCA. FTDNA's approach provides a statistical estimate, rather than a specific date.

In contrast, YFull bases haplogroup dating on the paper *Defining a New Rate Constant for Y-Chromosome SNPs based on Full Sequencing Data* by Adamov, Guryanov, Korzhavin, Tagankin, Urasin (2015). "YFull estimates the Most Common Ancestor (MCA) by first determining the TMRCA, which is based on the number of single nucleotide polymorphism (SNP) mutations and a specific mutation rate."[7]

Table 2 contains the currently available haplogroup dating by both FTDNA and YFull , as well as the FTDNA dating that was shared in the 2022 The Tipton Family Association of America Newsletter. Shift represents the difference in dating between 2022 and 2025.

[7] YFull. (n.d.). Retrieved September 1, 2025, from https://www.YFull.com/faq/what-yfulls-age-estimation-methodology/

Table 2: TMRCA Estimates by Method and Year

| | Shift (Years) | FTDNA Lower Limit (2025) | FTDNA Upper Limit (2025) | FTDNA Lower Limit (2022) | FTDNA Upper Limit (2022) | YFull Lower Limit (2025) | YFull Upper Limit (2025) |
|---|---|---|---|---|---|---|---|
| I-M253 (BCE) | | 11736 | 8548 | | | 3150 | 2050 |
| I-Y24812 (CE) | 101-123 | 1542 | 1735 | 1643 | 1858 | 1525 | 1875 |
| I-BY102911 (CE) | 69-106 | 1542 | 1735 | 1611 | 1841 | 1475 | 1900 |
| I-Y47457 (CE) | 16-157 | 1542 | 1735 | 1526 | 1892 | | |
| I-FTC81946 (CE) | 23-31 | 1636 | 1905 | 1659 | 1936 | | |
| I-Y17672 (CE) | 24-48 | 1472 | 1688 | 1496 | 1716 | 950 | 1625 |
| I-Y17673 (CE) | | 1542 | 1735 | | | | |

[8,9]

The TFDP offers insight into the evolving nature of Y-DNA science and serves as real-world evidence that incorporates results from both FTDNA and YFull. There have been three important advances in the FTDNA data since 2022. First, the TMRCA by FTDNA has been recalculated across the associated Tipton haplogroups between a range of 16 and 157 years, thus adding one to five generations. Second, I-Y17673 has been established. Third, I-Y17673 has been assigned an overlapping dating of I-Y17672 +70 years.

With interpretation of genealogical Y-DNA results, pitfalls include the failure to frame results within direct paternal lines, confusing haplogroups with ethnicity or nationality, overestimating time estimates, and confusing STRs and SNPs. Because the "order (of) the nine defining SNPs for haplogroup I-Y17672 occurred is not known,"[10] the present dating of I-Y17672 can potentially suggest false relationships or descendants belonging to an incorrect branch. If the estimation of the sequencing is incorrect, a misrepresentation of the TMRCA occurs. As expected with different methodologies, there is significant disagreement between the FTDNA and YFull databases in regards to the TMRCA of I-Y17672. YFull dates I-Y17672 about 63 to 522 years earlier than FTDNA. With 1620 being the beginning of The Great Migration, the range of I-Y17672 is so broad, 950 CE to 1688 CE depending on testing company and approach, it is difficult to predict whether I-Y17672 was formed in Colonial America or Europe. If I-Y17672 was created in Europe, it is plausible that participants outside of the project, whose families never migrated to North America, will match to I-Y17672.

[8] FTDNA. (n.d.). FTDNA Your Haplogroup Story:. Retrieved September 1, 2025, from https://discover.familytreedna.com/
[9] YFull. (n.d.). Haplogroup YTree v13.05.00 (09 August 2025). Retrieved September 1, 2025, from https://www.yfull.com/tree
[10] The Tipton Family Association of America. (2022). The Tipton Family Association of America Newsletter, Issue 44. Retrieved from https://tiptonfamilyassociationofamerica.com/wp-content/uploads/2022/12/Newsletter44_Fall_2022.pdf

## Conclusion

A subclade of the larger group (I), the precise global commonality of I-Y17672 is unknown. Unlike I-M253, testing has been limited to those who have participated in genealogical DNA studies. Within the dataset, the Tipton surname represents 79% of the men who have matched I-Y17672 and its subclades with a reported Tipton ancestry in the T-YDP and D-YDP. However, it is premature to conclude 79% of all I-Y17672 men globally are Tiptons as the currently tested population is remarkably small (n=24). Given 21% of the participants of T-YDP are of other surnames, any conclusion is premature. The eight men that have tested positive for I-Y17673 without sharing a genealogy could significantly change the surname results. As Y-DNA genealogical datasets grow with documented, versus predicted participants, study results will have significantly greater value in research. Until such point the science becomes repeatable and consistent across disciplines, we will continue to question the true relationship between Thomas Tipton and Jonathan Tipton.

Forensic, anthropological, and genealogical Y-DNA haplogroup dating methodologies produce disparate results. The significant TMRCA methodology disagreement between Y-DNA testing companies, and paucity of understanding of the population sizes of I-Y17672 and its subclades, make any chronological Y-DNA based conclusions premature. The dating of I-Y17673, and subclades I-Y24812, I-BY102911, and I-Y47457 in the TFDP has not reached a point aligning the autosomal-DNA and the Y-DNA results with significance.

Men that have tested to remarkably different early haplogroups, i.e. R-M269, could be removed from the TFDP. They and others in the 'unclassified' group are considerably unrelated. FTDNA project Y-DNA participants who have matched to I-M253, with a genealogically proven Tipton ancestor, represent a research opportunity. Testing at 700 markers would add specificity and possibly warrant their inclusion in future research. Y-DNA projects often assume a name-based project approach, however there may be greater utility employing a haplogroup based approach.

An unsourced independent genealogy should be weighted in a different way than a well-sourced or professionally researched genealogy in the projects. Of those participants who have shared a family history, incorporating a defined methodology to qualify the associated genealogical research would enhance the population analysis. It appears current genealogical Y-DNA testing is more effective at excluding relationships, rather than proving them, especially in the absence of traditional genealogical research.

About the author:

Scott Lytle is a member of the General Society of the War of 1812, the Sons of the Revolution in the State of New York, the National Society, Sons of the American Revolution, the Mayflower Society, and the Swedish Colonial Society. He holds a Master of Business Administration from the University of the Sciences in Philadelphia and a Master of Science in Bioethics from Columbia University in the City of New York. He is a member of the Surrogate Decision Making Committee for People with Special Needs in the State of New York, a member of the Empire State Bioethics Consortium, and a former member of the Bioethical Issues Committee for the New York City Bar Association. He has 25 years in the pharmaceutical industry.

Disclaimer: This independent research is based solely on publicly available and opted-in data from genetic genealogy projects. No private or identifiable participant information was accessed or disclosed. The analysis does not represent the views of FamilyTree DNA, YFull, or any affiliated institution. The conclusions are opinion and intended for genealogical exploration only. Any potential identification of individuals is unintentional and incidental. If any participant believes their data is misrepresented, they may contact the author for clarification or correction.